

REMARKS

The information contained in the computer readable form of Application No. 09/686,020 was prepared through the use of the software program "PatentIn" and was identical to that of the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of the changes made to the Specification by the current Amendment. The attached pages are captioned "**VERSION WITH MARKINGS TO SHOW CHANGES MADE.**"

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph beginning at line 25 of page 2 has been amended as follows:

In a related aspect, the invention provides an isolated polynucleotide that encodes, or is complementary to a sequence that encodes, the CCX CKR polypeptide. In some embodiments the polynucleotide has at least 10, 15, 25, 50 or 100 contiguous bases identical or exactly complementary to SEQ ID NO:1. In various embodiments, the polynucleotide is the full-length sequence of SEQ ID NO:1, encodes a CCX CKR polypeptide of the invention (e.g., having the sequence of SEQ ID NO:2 ~~SEQ ID:2~~ or a fragment thereof), or selectively hybridizes under high stringent hybridization conditions to a polynucleotide sequence of SEQ ID NO:1. The polynucleotide of the invention may be operably linked to a promoter. The invention provides recombinant vector (e.g., an expression vector) expressing the CCX CKR polypeptides of the invention. In one aspect, the invention provides a polynucleotide having sequence encoding a polypeptide that has an activity (e.g., a chemokine binding activity) of a CCX CKR polypeptide and which is (a) a polynucleotide having the sequence of SEQ ID NO:1 or SEQ ID NO:3 ~~SEQ ID NO:3~~; or (b) a polynucleotide which hybridizes under stringent conditions to (a); or (c) a polynucleotide sequence which is degenerate as a result of the genetic code to the sequences defined in (a) or (b).

Paragraph beginning at line 3 of page 5 has been amended as follows:

Figure 1 shows the nucleotide sequence for a human CCX CKR (SEQ ID NO:1) (~~SEQ ID NO:1~~) and the predicted amino acid sequence of the human CCX CKR polypeptide (SEQ ID NOS:2 and 12-14) (~~SEQ ID NO:2~~).

Paragraph beginning at line 7 of page 5 has been amended as follows:

Figure 2 shows the CCX CKR sequence aligned with those of other chemokine receptors, the expression pattern of CCX CKR RNA, and generation of a stable cell line expressing CCX CKR. Figure 2A shows sequence homology of the CCX CKR coding region (SEQ ID NO:2) with other chemokine receptors (SEQ ID NOS:6-9). Figure 2B shows cells and tissues expressing CCX CKR RNA, as analyzed by RT-PCR of cytoplasmic RNA from cultured primary cells and whole tissues from various organs as indicated. Figure 2C shows a population of transfected HEK-293 cells stably expressing CCX CKR protein containing an N-terminal Flag epitope, comparing intensity of anti-Flag mAb staining relative to wild type HEK293 cells.

Paragraph beginning at line 13 of page 6 has been amended as follows:

Figure 5 shows DNA sequence 5' to the translation start site of the CCX CKR gene (SEQ ID NOS:10 and 11), as determined from a genomic clone.

A circular postmark from the U.S. Patent and Trademark Office, Washington, D.C. The text "U.S. PATENT & TRADEMARK OFFICE" is at the bottom, "WASHINGTON, D.C." is in the middle, and "FEB 12 2002" is at the top.

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FEB 19 2002

TECH CENTER 1600/2900

SEQUENCE LISTING

<110> Mosling, Jennifer
Dairaghi, Daniel J.
Hanley, Michael
Miao, Zhenhua
Schall, Thomas J.
ChemoCentryx, Inc.

<120> Chemokine Receptor

<130> 019934-000710US

<140> US 09/686,020
<141> 2000-10-10

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1 5 10 15

gaa atg aat ggc act tat gac tac agt caa tat gaa ctg atc tgt atc	96
Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile	
20 25 30	

aaa gaa gat gtc aga gaa ttt gca aaa gtt ttc ctc cct gta ttc ctc 144
 Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
 35 40 45

aca ata gtt ttc gtc att gga ctt gca ggc aat tcc atg gta gtg gca	192		
Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala			
50	55	60	
att tat gcc tat tac aag aaa cag aga acc aaa aca gat gtg tac atc	240		
Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile			
65	70	75	80
ctg aat ttg gct gta gca gat tta ctc ctt cta ttc act ctg cct ttt	288		
Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Phe Thr Leu Pro Phe			
85	90	95	
tgg gct gtt aat gca gtt cat ggg tgg gtt tta ggg aaa ata atg tgc	336		
Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys			
100	105	110	
aaa ata act tca gcc ttg tac aca cta aac ttt gtc tct gga atg cag	384		
Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln			
115	120	125	
ttt ctg gct tgt atc agc ata gac aga tat gtg gca gta act aaa gtc	432		
Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val			
130	135	140	
ccc agc caa tca gga gtc gga aaa cca tgc tgg atc atc tgt ttc tgt	480		
Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys			
145	150	155	160
gtc tgg atg gct gcc atc ttg ctg agc ata ccc cag ctg gtt ttt tat	528		
Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr			
165	170	175	
aca gta aat gac aat gct agg tgc att ccc att ttc ccc cgc tac cta	576		
Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu			
180	185	190	
gga aca tca atg aaa gca ttg att caa atg cta gag atc tgc att gga	624		
Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly			
195	200	205	
ttt gta gta ccc ttt ctt att atg ggg gtc tgc tac ttt atc aca gca	672		
Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala			
210	215	220	
agg aca ctc atg aag atg cca aac att aaa ata tct cga ccc cta aaa	720		
Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys			
225	230	235	240
gtt ctg ctc aca gtc gtt ata gtt ttc att gtc act caa ctg cct tat	768		
Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr			
245	250	255	
aac att gtc aag ttc tgc cga gcc ata gac atc atc tac tcc ctg atc	816		
Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile			
260	265	270	
acc agc tgc aac atg agc aaa cgc atg gac atc gtc atc caa gtc aca	864		
Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr			
275	280	285	

gaa agc atc gca ctc ttt cac agc tgc ctc aac cca atc ctt tat gtt	912																																
Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val																																	
290	295		300	ttt atg gga gca tct ttc aaa aac tac gtt atg aaa gtg gcc aag aaa	960	Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys		305	310		315	320		tat ggg tcc tgg aga aga cag aga caa agt gtg gag gag ttt cct ttt	1008	Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe		325	330		335	gat tct gag ggt cct aca gag cca acc agt act ttt agc att taa	1053	Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile		340	345		350	aggtaaaaact gctctgcctt ttgcttggat acatatgaat gatgcttcc cctcaaataa	1113	aacatctgcc ttattctgaa aaaaaaaaaaa aaam	1147
	300																																
ttt atg gga gca tct ttc aaa aac tac gtt atg aaa gtg gcc aag aaa	960																																
Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys																																	
305	310		315	320		tat ggg tcc tgg aga aga cag aga caa agt gtg gag gag ttt cct ttt	1008	Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe		325	330		335	gat tct gag ggt cct aca gag cca acc agt act ttt agc att taa	1053	Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile		340	345		350	aggtaaaaact gctctgcctt ttgcttggat acatatgaat gatgcttcc cctcaaataa	1113	aacatctgcc ttattctgaa aaaaaaaaaaa aaam	1147								
	315																																
320																																	
tat ggg tcc tgg aga aga cag aga caa agt gtg gag gag ttt cct ttt	1008																																
Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe																																	
325	330		335	gat tct gag ggt cct aca gag cca acc agt act ttt agc att taa	1053	Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile		340	345		350	aggtaaaaact gctctgcctt ttgcttggat acatatgaat gatgcttcc cctcaaataa	1113	aacatctgcc ttattctgaa aaaaaaaaaaa aaam	1147																		
	335																																
gat tct gag ggt cct aca gag cca acc agt act ttt agc att taa	1053																																
Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile																																	
340	345		350	aggtaaaaact gctctgcctt ttgcttggat acatatgaat gatgcttcc cctcaaataa	1113	aacatctgcc ttattctgaa aaaaaaaaaaa aaam	1147																										
	350																																
aggtaaaaact gctctgcctt ttgcttggat acatatgaat gatgcttcc cctcaaataa	1113																																
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 <213> Homo sapiens
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 20 25 30
 Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
 35 40 45
 Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala
 50 55 60
 Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile
 65 70 75 80
 Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Phe Thr Leu Pro Phe
 85 90 95
 Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys
 100 105 110
 Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln
 115 120 125
 Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val
 130 135 140
 Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys
 145 150 155 160
 Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr
 165 170 175
 Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu
 180 185 190
 Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly
 195 200 205
 Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala
 210 215 220
 Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys
 225 230 235 240
 Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr
 245 250 255

25
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Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile
260 265 270
Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
275 280 285
Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
290 295 300
Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
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Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
340 345 350

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aaagtttcc cccctgtatt cctcacaata gtttgcgtca ttggacttgc aggcaattcc 180
atggtagtgg caatttatgc ctattacaag aaacagagaa cccaaacaga tgcgtacatc 240
ctgaatttgg ctgttagcaga tttactcctt ctattcactc tgccttttg ggctgttaat 300
gcagttcatg ggtgggtttt agggaaaata atgtcaaaa taacttcagc cttgtacaca 360
ctaaactttt tctcttggat gcagttctg gcttgtatca gcatagacag atatgtggca 420
gtaaactaaag tccccagcca atcaggagtg gggaaaaccat gctggatcat ctgtttctgt 480
gtctggatgg ctgccccat tttttttttt aacttagaa catcaatgaa agcatttgatt 540
aatgttaggt gcattccat tttccccgc aacttagaa catcaatgaa agcatttgatt 600
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cctacagacg caaccaggatc ttttagcatt taaaatgttggacttgc cttttgcttg 1080
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aaaaaaaaam 1147

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

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35 40 45

His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile Val Gly Ala Leu
50 55 60

Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys Thr Arg Val Lys
65 70 75 80

Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile Ala Asp Leu Leu
85 90 95

Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala Asp Gln Trp
100 105 110

Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser Met Tyr Lys Met
115 120 125

Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile Ser Val Asp Arg
130 135 140

Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr Trp Arg Glu Lys
145 150 155 160

Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile Trp Val Leu Ala
165 170 175

Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln Ile Lys Glu Glu
180 185 190

Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser Asp Glu Ser Thr
195 200 205

*a5
ant*

Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile Leu Gly Phe Phe
 210 215 220
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 245 250 255
 Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe Pro Tyr Asn Cys
 260 265 270
 Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met Phe Ile Ser Asn
 275 280 285
 Cys Ala Val Ser Thr Asn Ile Asp Ile Cys Phe Gln Val Thr Gln Thr
 290 295 300
 Ile Ala Phe Phe His Ser Cys Leu Asn Pro Val Leu Tyr Val Phe Val
 305 310 315 320
 Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu Lys Asn Leu Gly
 325 330 335
 Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg Arg Glu Gly Ser
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 Leu

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 35 40 45
 Ser Lys Lys Asp Val Arg Asn Phe Lys Ala Trp Phe Leu Pro Ile Met
 50 55 60
 Tyr Ser Ile Ile Cys Phe Val Gly Leu Leu Gly Asn Gly Leu Val Val
 65 70 75 80
 Leu Thr Tyr Ile Tyr Phe Lys Arg Leu Lys Thr Met Thr Asp Thr Tyr
 85 90 95

Leu Leu Asn Leu Ala Val Ala Asp Ile Leu Phe Leu Leu Thr Leu Pro
 100 105 110
 Phe Trp Ala Tyr Ser Ala Ala Lys Ser Trp Val Phe Gly Val His Phe
 115 120 125
 Cys Lys Leu Ile Phe Ala Ile Tyr Lys Met Ser Phe Phe Ser Gly Met
 130 135 140
 Leu Leu Leu Leu Cys Ile Ser Ile Asp Arg Tyr Val Ala Ile Val Gln
 145 150 155 160
 Ala Val Ser Ala His Arg His Arg Ala Arg Val Leu Leu Ile Ser Lys
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 Leu Ser Cys Val Gly Ser Ala Ile Leu Ala Thr Val Leu Ser Ile Pro
 180 185 190
 Glu Leu Leu Tyr Ser Asp Leu Gln Arg Ser Ser Ser Glu Gln Ala Met
 195 200 205
 Arg Cys Ser Leu Ile Thr Glu His Val Glu Ala Phe Ile Thr Ile Gln
 210 215 220
 Val Ala Gln Met Val Ile Gly Phe Leu Val Pro Leu Leu Ala Met Ser
 225 230 235 240
 Phe Cys Tyr Leu Val Ile Ile Arg Thr Leu Leu Gln Ala Arg Asn Phe
 245 250 255
 Glu Arg Asn Lys Ala Ile Lys Val Ile Ile Ala Val Val Val Phe
 260 265 270
 Ile Val Phe Gln Leu Pro Tyr Asn Gly Val Val Leu Ala Gln Thr Val
 275 280 285
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 Asn Ile Ala Tyr Asp Val Thr Tyr Ser Leu Ala Cys Val Arg Cys Cys
 305 310 315 320
 Val Asn Pro Phe Leu Tyr Ala Phe Ile Gly Val Lys Phe Arg Asn Asp
 325 330 335
 Ile Phe Lys Leu Phe Lys Asp Leu Gly Cys Leu Ser Gln Glu Gln Leu
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 Glu Ala Glu Thr Thr Thr Phe Ser Pro
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35 40 45

Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn
50 55 60

Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met
65 70 75 80

Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val
85 90 95

Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val
100 105 110

Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn
115 120 125

Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr
130 135 140

Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr
145 150 155 160

Leu Pro Arg Thr Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val
165 170 175

Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln
180 185 190

Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile
195 200 205

Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe
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Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr
225 230 235 240

Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile
245 250 255

Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met
260 265 270

Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys
275 280 285

Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu
290 295 300

Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly
 305 310 315 320
 Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys
 325 330 335
 Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr
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 355 360 365
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 35 40 45
 Asn Ser Leu Val Leu Val Ile Ser Ile Phe Tyr His Lys Leu Gln Ser
 50 55 60
 Leu Thr Asp Val Phe Leu Val Asn Leu Pro Leu Ala Asp Leu Val Phe
 65 70 75 80
 Val Cys Thr Leu Pro Phe Trp Ala Tyr Ala Gly Ile His Glu Trp Val
 85 90 95
 Phe Gly Gln Val Met Cys Lys Ser Leu Leu Gly Ile Tyr Thr Ile Asn
 100 105 110
 Phe Tyr Thr Ser Met Leu Ile Leu Thr Cys Ile Thr Val Asp Arg Phe
 115 120 125
 Ile Val Val Val Lys Ala Thr Lys Ala Tyr Asn Gln Gln Ala Lys Arg
 130 135 140
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 145 150 155 160
 Leu Val Ser Leu Pro Gln Ile Ile Tyr Gly Asn Val Phe Asn Leu Asp
 165 170 175
 Lys Leu Ile Cys Gly Tyr His Asp Glu Ala Ile Ser Thr Val Val Leu
 180 185 190

Ala Thr Gln Met Thr Leu Gly Phe Phe Leu Pro Leu Leu Thr Met Ile
 195 200 205
 Val Cys Tyr Ser Val Ile Ile Lys Thr Leu Leu His Ala Gly Gly Phe
 210 215 220
 Gln Lys His Arg Ser Leu Lys Ile Ile Phe Leu Val Met Ala Val Phe
 225 230 235 240
 Leu Leu Thr Gln Met Pro Phe Asn Leu Met Lys Phe Ile Arg Ser Thr
 245 250 255
 His Trp Glu Tyr Tyr Ala Met Thr Ser Phe His Tyr Thr Ile Met Val
 260 265 270
 Thr Glu Ala Ile Ala Tyr Leu Arg Ala Cys Leu Asn Pro Val Leu Tyr
 275 280 285
 Ala Phe Val Ser Leu Lys Phe Arg Lys Asn Phe Trp Lys Leu Val Lys
 290 295 300
 Asp Ile Gly Cys Leu Pro Tyr Leu Gly Val Ser His Gln Trp Lys Ser
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 Thr Ser Met Phe Gln Leu
 340

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 <213> Homo sapiens

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 start site of CCX CKR

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 aaataaaacca agtaatttgc tattttcggt ttttattcaat ttgttgtaga tatactttta 180
 cgattcacaa aatttatgtat gtaaaagatta taacactatt tattttttt agttaaaaatc 240
 taattaaattt ttcataatttt aaaaatcatt tttacataaa agtcttcact tttattttagg 300
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<220>
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cont
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